



1

SEQUENCE LISTING

<110> SHERMAN, LINDA A.
LUSTGARTEN, JOSEPH

<120> RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS
SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

<130> 46147/55793

<140> 08/812,393
<141> 1997-03-05

<160> 64

<170> PatentIn Ver. 2.1

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MAY 14 2003

TECH CENTER 1600/2900

<210> 1
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1332)

<220>
<223> Description of Artificial Sequence: Synthetic
single chain TCR derivative nucleotide sequence

<400> 1
ctc gag atg cag agg aac ctg gga gct gtg ctg ggg att ctg tgg gtg 48
Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
1 5 10 15

cag att tgc tgg ctg aaa gaa cag caa gtg cag cag agt ccc gca tcc 96
Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
20 25 30

ttg gtt ctg cag gag ggg gag aac gca gag ctc cag tgt agc ttt tcc 144
Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
35 40 45

atc ttt aca aac cag gtg cag tgg ttt tac caa cgt cct ggg gga aga 192
Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
50 55 60

ctc gtc agc ctg ttg tac aat cct tct ggg aca aag cag agt ggg aga 240
Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
65 70 75 80

ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att 288
Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
85 90 95

tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat 336
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
100 105 110

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tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
115 120 125

384

tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt
Ser Val Lys Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
130 135 140

432

gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
145 150 155 160

480

gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
165 170 175

528

aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
180 185 190

576

atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
195 200 205

624

gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
210 215 220

672

ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
225 230 235 240

720

ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
245 250 255

768

ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
260 265 270

816

ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Pro Ala Pro Arg Pro
275 280 285

864

cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
290 295 300

912

tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
305 310 315 320

960

ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
325 330 335

1008

agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc	1056																																																																	
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu																																																																		
340	345	350				tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac	1104	Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp		355	360	365				aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag	1152	Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys		370	375	380				aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg	1200	Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala		385	390	395	400			gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag	1248	Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys		405	410	415				ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296	Gly His Asp Gly Leu Tyr Gln Gly Ile Ser Thr Ala Thr Lys Asp Thr		420	425	430				tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344	Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		435	440				acc gcg	1350
350																																																																		
tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac	1104																																																																	
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp																																																																		
355	360	365				aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag	1152	Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys		370	375	380				aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg	1200	Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala		385	390	395	400			gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag	1248	Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys		405	410	415				ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296	Gly His Asp Gly Leu Tyr Gln Gly Ile Ser Thr Ala Thr Lys Asp Thr		420	425	430				tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344	Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		435	440				acc gcg	1350										
365																																																																		
aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag	1152																																																																	
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys																																																																		
370	375	380				aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg	1200	Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala		385	390	395	400			gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag	1248	Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys		405	410	415				ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296	Gly His Asp Gly Leu Tyr Gln Gly Ile Ser Thr Ala Thr Lys Asp Thr		420	425	430				tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344	Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		435	440				acc gcg	1350																				
380																																																																		
aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg	1200																																																																	
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala																																																																		
385	390	395	400			gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag	1248	Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys		405	410	415				ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296	Gly His Asp Gly Leu Tyr Gln Gly Ile Ser Thr Ala Thr Lys Asp Thr		420	425	430				tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344	Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		435	440				acc gcg	1350																														
395	400																																																																	
gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag	1248																																																																	
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys																																																																		
405	410	415				ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296	Gly His Asp Gly Leu Tyr Gln Gly Ile Ser Thr Ala Thr Lys Asp Thr		420	425	430				tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344	Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		435	440				acc gcg	1350																																								
415																																																																		
ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296																																																																	
Gly His Asp Gly Leu Tyr Gln Gly Ile Ser Thr Ala Thr Lys Asp Thr																																																																		
420	425	430				tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344	Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		435	440				acc gcg	1350																																																		
430																																																																		
tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344																																																																	
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg																																																																		
435	440																																																																	
acc gcg	1350																																																																	

<210> 2

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
single chain TCR protein

<400> 2

Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val			
1	5	10	15
10	15		

Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser			
20	25	30	
30			

Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser			
35	40	45	
45			

Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg			
50	55	60	
60			

Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg			
65	70	75	80
75	80		

Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile			
85	90	95	
95			

Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
 100 105 110
 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
 115 120 125
 Ser Val Lys Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly
 130 135 140
 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
 145 150 155 160
 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
 165 170 175
 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
 180 185 190
 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
 195 200 205
 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
 210 215 220
 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 225 230 235 240
 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
 245 250 255
 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
 260 265 270
 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
 275 280 285
 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
 290 295 300
 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
 305 310 315 320
 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
 325 330 335
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 340 345 350
 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 355 360 365
 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Lys Pro Arg Arg Lys
 370 375 380
 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 385 390 395 400

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
405 410 415
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
420 425 430
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
435 440

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 3
cccaaggcac tgatgttcat cttc 24

<210> 4
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 4
tgagacaaag tccccaatct ctgacag 27

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
ctgcagctgc tcctcaagta ctattc 26

<210> 6
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
tcccggagaa ggtccacagt tcctttt 28

<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
gaagcagcag agggttgaa gccacatac 29

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
ggcaggttt cagttgttta tgaaggt 27

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
gttcctttt cagggtccag aatatgt 27

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
gcgaagaact caccctggac tggcat 27

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
gagctccaca gacaacaaga ggacgcagca 30

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
gagctgcgac gttccttagt gactgtg 27

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
cctcgtcagc ctgttgtcca atccttctgg 30

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
cagecctcatc aatctgttct acttggct 28

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
ccaccaggga ccacagttt a tcattcaa 28

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
acctggagag aatcctaagg tcatacat 27

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
aggctttgtg tccctgacag tcctggtt 28

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
caagcaaaca ctgttagtgca gagccttcc 30

<210> 19
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
caagacatcc ataactgcc tacag 25

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
gtgtatgaaa cccaggacag ttcttac 27

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
ccgtatttct ttcttatgtt gttttggat 29

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
caaagctctc catcgctgac tttcaag 28

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
atctaattctt gggaaagagca aat 23

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
ggcgtctggt accacgtggt caa 23

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
gtgaaaagggc aaggacaaaa agc 23

<210> 26
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gatatgcgaa cagtatctag gc 22

<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
acataatcaa aggaaaggaa gaa 23

<210> 28
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 28
tcctgatgg tcaggaaggg caa 23

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 29
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<210> 30
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 30
ataaccatga caatatgtac tgg 23

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
ataaccacaa caacatgtac tgg 23

<210> 32
<211> 23
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<220>
<223> Description of Artificial Sequence: Primer

<400> 32
atagccacaa ctacatgtac tgg 23

<210> 33
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 33
agcttgcaag agttggaaaa cca 23

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
gattatgtt agctacaata ata 23

<210> 35
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 35
acaaggtgac aggaaaggga caa 23

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
acctacagaa cccaggact cag 23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
cagttgcctt cggatcgatt ttc 23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
gccgagatca aggctgtggg cag 23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
agaaccatct gtaagagtgg aac 23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 40		
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<210> 41		
<211> 23		
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<210> 42		
<211> 22		
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<220>		
<223> Description of Artificial Sequence: Primer		
<400> 42		
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<210> 43		
<211> 393		
<212> DNA		
<213> Homo sapiens		
<220>		
<221> CDS		
<222> (1)..(393)		
<400> 43		
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Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn		
1 5 10 15		
tgg gtg cag agc cag aag gtg cag cag agc cca gaa tcc ctc agt	96	
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser		
20 25 30		
gtc cca gag gga ggc atg gcc tct ctc aac tgc act tca agt gat cgc	144	
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg		
35 40 45		
aat ttt cag tat ttc tgg tgg tac aga cag cat tct gga gaa ggc ccc	192	
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro		
50 55 60		
aaa gca ctg atg tcc atc ttc tct gat ggt gac aag aaa gaa ggc aga	240	
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg		
65 70 75 80		

ttc aca gct cac ctc aat aag gcc agc ctg cat gtt tcc ctg cac atc 288
 Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
 85 90 95

aga gac tcc cag ccc agt gac tcc gct ctc tac ttc tgt gca gtt atg 336
 Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
 100 105 110

gat tat aac cag ggg aag ctt atc ttt ggg cag ggt acc aag tta tct 384
 Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
 115 120 125

atc aag ccc 393
 Ile Lys Pro
 130

<210> 44
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
 1 5 10 15

Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
 20 25 30

Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
 35 40 45

Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
 50 55 60

Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
 65 70 75 80

Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
 85 90 95

Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
 100 105 110

Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
 115 120 125

Ile Lys Pro
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<210> 45
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)..(402)

<400> 45

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Met	Gly	Ser	Arg	Leu	Phe	Phe	Val	Val	Leu	Ile	Leu	Leu	Cys	Ala	Lys
1				5				10				15			

cac	atg	gag	gct	gca	gtc	acc	caa	agt	cca	aga	agc	aag	gtg	gca	gta	96
His	Met	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Ser	Lys	Val	Ala	Val	
						20		25				30				

aca	gga	gga	aag	gtg	aca	ttg	agc	tgt	cac	cag	act	aat	aac	cat	gac	144
Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	His	Gln	Thr	Asn	Asn	His	Asp	
						35		40			45					

tat	atg	tac	tgg	tat	cg	cag	gac	acg	ggg	cat	ggg	ctg	agg	ctg	atc	192
Tyr	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Thr	Gly	His	Gly	Leu	Arg	Leu	Ile	
						50		55			60					

cat	tac	tca	tat	gtc	gct	gac	agc	acg	gag	aaa	gga	gat	atc	cct	gat	240
His	Tyr	Ser	Tyr	Val	Ala	Asp	Ser	Thr	Glu	Lys	Gly	Asp	Ile	Pro	Asp	
						65		70			75		80			

ggg	tac	aag	gcc	tcc	aga	cca	agc	caa	gag	aat	ttc	tct	ctc	att	ctg	288
Gly	Tyr	Lys	Ala	Ser	Arg	Pro	Ser	Gln	Glu	Asn	Phe	Ser	Leu	Ile	Leu	
						85		90			95					

gag	ttg	gct	tcc	ctt	tct	cag	tca	gct	gta	tat	ttc	tgt	gcc	agc	agc	336
Glu	Leu	Ala	Ser	Leu	Ser	Gln	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Ser	Ser	
						100		105			110					

gat	ttc	gcc	ggg	aca	ggg	ggc	ttc	tat	gaa	cag	tac	ttc	ggt	ccc	ggc	384
Asp	Phe	Ala	Gly	Thr	Gly	Gly	Phe	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	
						115		120			125					

acc	agg	ctc	acg	gtt	tct											402
Thr	Arg	Leu	Thr	Val	Ser											
					130											

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Met	Gly	Ser	Arg	Leu	Phe	Phe	Val	Val	Leu	Ile	Leu	Leu	Cys	Ala	Lys
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His	Met	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Ser	Lys	Val	Ala	Val
						20		25			30				

Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	His	Gln	Thr	Asn	Asn	His	Asp
						35		40			45				

Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
50 55 60

His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
65 70 75 80

Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
85 90 95

Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
100 105 110

Asp Phe Ala Gly Thr Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
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Thr Arg Leu Thr Val Ser
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